

## SEQUENCE LISTING

<110> Nakamura, Yusuke  
Furukawa, Yoichi

<120> METHOD FOR DIAGNOSING HEPATOCELLULAR  
CARCINOMAS

<130> 082368-007600US

<150> PCT/JP2004/013722  
<151> 2004-09-14

<150> US 60/505,632  
<151> 2003-09-24

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 1528  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (133) ... (1308)

<400> 1  
ccacgcgtcc gcgggagcgg agccgtggcg cgctcgcccc ggacgcggc cgccccctccg 60  
ctcgccctac tgagcgagcg gcccggggcg ccgagggtc cgcgcgcgc ggggcgcacc 120  
gcctggccg cc atg tgc tcc cag ctc tgg ttc ctg acg gac cgg cgc atc 171  
Met Cys Ser Gln Leu Trp Phe Leu Thr Asp Arg Arg Ile  
1 5 10  
cgc gag gac tac ccg cag gtg cag atc ctg cgc gcc ctc cgg cag cgc 219  
Arg Glu Asp Tyr Pro Gln Val Gln Ile Leu Arg Ala Leu Arg Gln Arg  
15 20 25  
tgc tcc gag cag gac gtg cgc ttc cgg gcg gtg ctt atg gac cag atc 267  
Cys Ser Glu Gln Asp Val Arg Phe Arg Ala Val Leu Met Asp Gln Ile  
30 35 40 45  
gcc gtc acc atc gtc ggc ggc cac ctc ggc ctc cag cta aac cag aag 315  
Ala Val Thr Ile Val Gly Gly His Leu Gly Leu Gln Leu Asn Gln Lys  
50 55 60  
gcc ctc acc act ttc ccg gat gtg gtg ctt gta cgg gta ccc aca ccc 363  
Ala Leu Thr Thr Phe Pro Asp Val Val Leu Val Arg Val Pro Thr Pro  
65 70 75  
tca gtg cag tca gac agt gac atc act gtc ctg cga cac ctg gag aag 411  
Ser Val Gln Ser Asp Ser Asp Ile Thr Val Leu Arg His Leu Glu Lys  
80 85 90  
ctg ggc tgc cgg ttg gtc aat cgc cca cag agc atc tta aat tgc atc 459  
Leu Gly Cys Arg Leu Val Asn Arg Pro Gln Ser Ile Leu Asn Cys Ile  
95 100 105

aac aaa ttc tgg acg ttc caa gaa ctg gct gga cat ggg gtc ccc atg			507
Asn Lys Phe Trp Thr Phe Gln Glu Leu Ala Gly His Gly Val Pro Met			
110	115	120	125
cca gac acc ttc tcc tat ggt ggg cat gaa gac ttt tca aaa atg att			555
Pro Asp Thr Phe Ser Tyr Gly Gly His Glu Asp Phe Ser Lys Met Ile			
130	135	140	
gat gaa gct gag ccc ctg ggc tac cca gtc gtg gtg aag agc aca cga			603
Asp Glu Ala Glu Pro Leu Gly Tyr Pro Val Val Val Lys Ser Thr Arg			
145	150	155	
ggc cac cgg gga aaa gct gtt ttt ctg gca aga gat aaa cat cac ctc			651
Gly His Arg Gly Lys Ala Val Phe Leu Ala Arg Asp Lys His His Leu			
160	165	170	
tct gac atc tgc cat ctg atc cgc cac gat gtg ccc tac ctg ttc cag			699
Ser Asp Ile Cys His Leu Ile Arg His Asp Val Pro Tyr Leu Phe Gln			
175	180	185	
aag tac gtg aag gag tcc cat gga aag gac atc cgg gtg gtg gtg gta			747
Lys Tyr Val Lys Glu Ser His Gly Lys Asp Ile Arg Val Val Val Val			
190	195	200	205
ggg ggc cag gtc ata ggc tct atg ctt cgc tgc tcc act gat gga cgg			795
Gly Gly Gln Val Ile Gly Ser Met Leu Arg Cys Ser Thr Asp Gly Arg			
210	215	220	
atg cag agc aac tgc tct ctc ggt ggc gtg ggc gtc aag tgt ccg ctg			843
Met Gln Ser Asn Cys Ser Leu Gly Gly Val Gly Val Lys Cys Pro Leu			
225	230	235	
aca gaa caa ggc aag cag ttg gct att cag gtg tcc aac atc cta ggc			891
Thr Glu Gln Gly Lys Gln Leu Ala Ile Gln Val Ser Asn Ile Leu Gly			
240	245	250	
atg gac ttc tgt ggc att gat ctc ctt atc atg gac gat ggc tcc ttt			939
Met Asp Phe Cys Gly Ile Asp Leu Leu Ile Met Asp Asp Gly Ser Phe			
255	260	265	
gtg gtg tgt gag gca aat gct aat gtt ggc ttc cta gcc ttt gac cag			987
Val Val Cys Glu Ala Asn Ala Asn Val Gly Phe Leu Ala Phe Asp Gln			
270	275	280	285
gca tgc aac tta gat gtg ggt ggg atc att gca gac tat acc atg tcc			1035
Ala Cys Asn Leu Asp Val Gly Gly Ile Ile Ala Asp Tyr Thr Met Ser			
290	295	300	
ttg ctg cca aat agg cag act gga aag atg gct gtc ctc cca gga ctg			1083
Leu Leu Pro Asn Arg Gln Thr Gly Lys Met Ala Val Leu Pro Gly Leu			
305	310	315	
tcg agt cca agg gag aag aac gag ccg gat ggc tgt gct tca gct cag			1131
Ser Ser Pro Arg Glu Lys Asn Glu Pro Asp Gly Cys Ala Ser Ala Gln			
320	325	330	
gga gtt gca gag agc gtc tat acc atc aac agt ggg tct acc tct agc			1179
Gly Val Ala Glu Ser Val Tyr Thr Ile Asn Ser Gly Ser Thr Ser Ser			
335	340	345	

gaa agt gag cct gaa ctg gga gag atc cgg gat tcc tca gca agc aca 1227  
 Glu Ser Glu Pro Glu Leu Gly Glu Ile Arg Asp Ser Ser Ala Ser Thr  
 350 355 360 365  
  
 atg ggg gcc cca ccc tcc atg ctg ccc gaa cct ggc tac aac att aac 1275  
 Met Gly Ala Pro Pro Ser Met Leu Pro Glu Pro Gly Tyr Asn Ile Asn  
 370 375 380  
  
 aac agg att gct tct gag tta aaa ctt aag tga attcctgctt tttggcagca 1328  
 Asn Arg Ile Ala Ser Glu Leu Lys Leu Lys  
 385 390  
  
 tttaaaccaa atcctactgc ttccctagta gtttgagtg aataaaatct ggactaatgt 1388  
 gatttcattt gcacagaaac tagaaatccc atctggcac tcagcatttt ttctaacat 1448  
 gatttaagca aatggcctag ctttgtggtt ttacaaaga caaatataaa aacactcaca 1508  
 agaacaaaaa aaaaaaaaaa 1528  
  
 <210> 2  
 <211> 391  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 2  
 Met Cys Ser Gln Leu Trp Phe Leu Thr Asp Arg Arg Ile Arg Glu Asp  
 1 5 10 15  
 Tyr Pro Gln Val Gln Ile Leu Arg Ala Leu Arg Gln Arg Cys Ser Glu  
 20 25 30  
 Gln Asp Val Arg Phe Arg Ala Val Leu Met Asp Gln Ile Ala Val Thr  
 35 40 45  
 Ile Val Gly Gly His Leu Gly Leu Gln Leu Asn Gln Lys Ala Leu Thr  
 50 55 60  
 Thr Phe Pro Asp Val Val Leu Val Arg Val Pro Thr Pro Ser Val Gln  
 65 70 75 80  
 Ser Asp Ser Asp Ile Thr Val Leu Arg His Leu Glu Lys Leu Gly Cys  
 85 90 95  
 Arg Leu Val Asn Arg Pro Gln Ser Ile Leu Asn Cys Ile Asn Lys Phe  
 100 105 110  
 Trp Thr Phe Gln Glu Leu Ala Gly His Gly Val Pro Met Pro Asp Thr  
 115 120 125  
 Phe Ser Tyr Gly Gly His Glu Asp Phe Ser Lys Met Ile Asp Glu Ala  
 130 135 140  
 Glu Pro Leu Gly Tyr Pro Val Val Val Lys Ser Thr Arg Gly His Arg  
 145 150 155 160  
 Gly Lys Ala Val Phe Leu Ala Arg Asp Lys His His Leu Ser Asp Ile  
 165 170 175  
 Cys His Leu Ile Arg His Asp Val Pro Tyr Leu Phe Gln Lys Tyr Val  
 180 185 190  
 Lys Glu Ser His Gly Lys Asp Ile Arg Val Val Val Val Gly Gly Gln  
 195 200 205  
 Val Ile Gly Ser Met Leu Arg Cys Ser Thr Asp Gly Arg Met Gln Ser  
 210 215 220  
 Asn Cys Ser Leu Gly Gly Val Gly Val Lys Cys Pro Leu Thr Glu Gln  
 225 230 235 240  
 Gly Lys Gln Leu Ala Ile Gln Val Ser Asn Ile Leu Gly Met Asp Phe  
 245 250 255  
 Cys Gly Ile Asp Leu Leu Ile Met Asp Asp Gly Ser Phe Val Val Cys  
 260 265 270  
 Glu Ala Asn Ala Asn Val Gly Phe Leu Ala Phe Asp Gln Ala Cys Asn  
 275 280 285  
 Leu Asp Val Gly Gly Ile Ile Ala Asp Tyr Thr Met Ser Leu Leu Pro  
 290 295 300

Asn Arg Gln Thr Gly Lys Met Ala Val Leu Pro Gly Leu Ser Ser Pro  
305 310 315 320  
Arg Glu Lys Asn Glu Pro Asp Gly Cys Ala Ser Ala Gln Gly Val Ala  
325 330 335  
Glu Ser Val Tyr Thr Ile Asn Ser Gly Ser Thr Ser Ser Glu Ser Glu  
340 345 350  
  
Pro Glu Leu Gly Glu Ile Arg Asp Ser Ser Ala Ser Thr Met Gly Ala  
355 360 365  
Pro Pro Ser Met Leu Pro Glu Pro Gly Tyr Asn Ile Asn Asn Arg Ile  
370 375 380  
Ala Ser Glu Leu Lys Leu Lys  
385 390

<210> 3  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> An artificially synthesized primer sequence for  
RT-PCR

<400> 3  
acaacagccct caagatcatc ag 22

<210> 4  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> An artificially synthesized primer sequence for  
RT-PCR

<400> 4  
ggtccaccac tgacacgttg 20

<210> 5  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> An artificially synthesized primer sequence for  
RT-PCR

<400> 5  
caaataggca gactggaaag atg 23

<210> 6  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> An artificially synthesized primer sequence for  
RT-PCR

<400> 6

ctagggaagc agtaggattt ggt	23
<210> 7	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> An artificially synthesized primer sequence for	
RT-PCR	
<400> 7	
attgtcgacg ctcgcctac tgagcgagcg	30
<210> 8	
<211> 36	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> An artificially synthesized primer sequence for	
RT-PCR	
<400> 8	
aatctcgaga gcaggaattc acttaagttt taactc	36
<210> 9	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> An artificially synthesized primer sequence for	
RT-PCR	
<400> 9	
tggtagccaa gtgcaggta ta	22
<210> 10	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> An artificially synthesized primer sequence for	
RT-PCR	
<400> 10	
ccaaagggtt tctgcagttt ca	22
<210> 11	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> An artificially synthesized primer sequence for	
RT-PCR	
<400> 11	
tgcggatcca gagcagattt tactgagagt	30

<210> 12		
<211> 29		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> An artificially synthesized primer sequence for		
RT-PCR		
<400> 12		
ctcttatctcg agtgaggcgg aaagaacca	29	
<210> 13		
<211> 47		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> An artificially synthesized primer sequence for		
RT-PCR		
<400> 13		
tttaagcttg aagaccattt ttggaaaaaaaaaaaaaaaaa aaaaaaac	47	
<210> 14		
<211> 34		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> An artificially synthesized primer sequence for		
RT-PCR		
<400> 14		
tttaagcttg aagacatggg aaagagtggt ctca	34	
<210> 15		
<211> 51		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> An artificially synthesized oligonucleotide		
sequence for siRNA		
<400> 15		
caccgaagca gcacgacttc ttcttcaaga gagaagaagt cgtgctgctt c	51	
<210> 16		
<211> 51		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> An artificially synthesized oligonucleotide		
sequence for siRNA		
<400> 16		
aaaagaagca gcacgacttc ttctctttt aagaagaagt cgtgctgctt c	51	

```

<210> 17
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> An artificially synthesized oligonucleotide
      sequence for siRNA

<400> 17
tccccgtgtcc gctgacagaa caattcaaga gattgttctg tcagcggaca c      51

<210> 18
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> An artificially synthesized oligonucleotide
      sequence for siRNA

<400> 18
aaaagtgtcc gctgacagaa caatctcttg aattgttctg tcagcggaca c      51

<210> 19
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> An artificially synthesized target sequence for
      siRNA

<400> 19
gtgtcccgctg acagaacaa                                         19

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> An artificially synthesized primer sequence for
      RT-PCR

<400> 20
gagctcctga accatctgct c                                         21

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> An artificially synthesized primer sequence for
      RT-PCR

<400> 21
caagatgtac agagcatcac agc                                         23

<210> 22

```

<211> 29		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> An artificially synthesized primer sequence for		
RT-PCR		
<400> 22		
attgaattcg catggcgcca cccgcggcg		29
<210> 23		
<211> 32		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> An artificially synthesized primer sequence for		
RT-PCR		
<400> 23		
aatggtacctt caccaaggcc tccagacact cc		32
<210> 24		
<211> 51		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> An artificially synthesized oligonucleotide		
sequence for siRNA		
<400> 24		
tcccaactttt agggaccctg cagttcaaga gactgcaggg tccctaaaag t		51
<210> 25		
<211> 51		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> An artificially synthesized oligonucleotide		
sequence for siRNA		
<400> 25		
aaaaaactttt agggaccctg cagtctttt aactgcaggg tccctaaaag t		51
<210> 26		
<211> 19		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> An artificially synthesized target sequence for		
siRNA		
<400> 26		
acttttaggg accctgcag		19
<210> 27		
<211> 1375		

<212> DNA  
<213> Homo sapiens

<220>

<221> CDS

<222> (125) ... (799)

<400> 27

ggagcgcgga cggctggct gctgctggc ggccgcgggg cagcggaggg cgccggcact 60  
ccggcccccc cccgctcccccc tccccctgc tccttagcccc tgccgcgtcc cccggcggagc 120  
gggc atg gcg cca ccc gcg gct ggc gac cgt gtg ggc cgt gag 169  
Met Ala Pro Pro Ala Ala Pro Gly Arg Asp Arg Val Gly Arg Glu  
1 5 10 15

gat gag gac ggc tgg gag acg cga ggg gac cgc aag gcc cgg aag ccc 217  
Asp Glu Asp Gly Trp Glu Thr Arg Gly Asp Arg Lys Ala Arg Lys Pro  
20 25 30

ctg gtg gag aag aag cgg cgc cgg atc aac gag agc ctg cag gag 265  
Leu Val Glu Lys Lys Arg Arg Ala Arg Ile Asn Glu Ser Leu Gln Glu  
35 40 45

ctg cgg ctg ctg ctg gcg ggc gcc gag gtg cag gcc aag ctg gag aac 313  
Leu Arg Leu Leu Ala Gly Ala Glu Val Gln Ala Lys Leu Glu Asn  
50 55 60

gcc gaa gtg ctg gag ctg acg gtg cgg cgg gtc cag ggt gtg ctg cgg 361  
Ala Glu Val Leu Glu Leu Thr Val Arg Arg Val Gln Gly Val Leu Arg  
65 70 75

ggc cgg cgc ggc gag cgc gag cag ctg cag gcg gaa gcg agc gag cgc 409  
Gly Arg Ala Arg Glu Glu Gln Leu Gln Ala Glu Ala Ser Glu Arg  
80 85 90 95

ttc gct gcc ggc tac atc cag tgc atg cac gag gtg cac acg ttc gtg 457  
Phe Ala Ala Gly Tyr Ile Gln Cys Met His Glu Val His Thr Phe Val  
100 105 110

tcc acg tgc cag gcc atc gac gct acc gtc gct gcc gag ctc ctg aac 505  
Ser Thr Cys Gln Ala Ile Asp Ala Thr Val Ala Ala Glu Leu Leu Asn  
115 120 125

cat ctg ctc gag tcc atg ccg ctg cgt gag ggc agc agc ttc cag gat 553  
His Leu Leu Glu Ser Met Pro Leu Arg Glu Gly Ser Ser Phe Gln Asp  
130 135 140

ctg ctg ggg gac gcc ctg gcg ggg cca cct aga gcc cct gga cgg agt 601  
Leu Leu Gly Asp Ala Leu Ala Gly Pro Pro Arg Ala Pro Gly Arg Ser  
145 150 155

ggc tgg cct gcg ggg ggc gct ccg gga tcc cca ata ccc agc ccc ccg 649  
Gly Trp Pro Ala Gly Ala Pro Gly Ser Pro Ile Pro Ser Pro Pro  
160 165 170 175

ggt cct ggg gac gac ctg tgc tcc gac ctg gag gag gcc cct gag gct 697  
Gly Pro Gly Asp Asp Leu Cys Ser Asp Leu Glu Ala Pro Glu Ala  
180 185 190

gaa ctg agt cag gct cct gct gag ggg ccc gac ttg gtg ccc gca gcc 745  
Glu Leu Ser Gln Ala Pro Ala Glu Gly Pro Asp Leu Val Pro Ala Ala  
195 200 205

ctg ggc agc ctg acc aca gcc caa att gcc cgg agt gtc tgg agg cct 793  
Leu Gly Ser Leu Thr Thr Ala Gln Ile Ala Arg Ser Val Trp Arg Pro  
210 215 220

tgg tga ccaatgccag ccagagtcct gcgggggtgg gcccggccct ccctggatct 849  
Trp \*

cctccctcct cccaggggtt cagatgttgtt ggggttagggc cctggaaagtc tcccagggtct 909  
tccctccctc ctctgatgga tggcttgcag ggcagccct ggttaaccagc ccagtcagc 969  
cccagccccg tttcttaaga aacttttagg gaccctgcag ctctggagtg ggtggaggg 1029  
gggagctacg ggcaggagga agaattttgt agagctgcca ggcgtctccc aggttcaccc 1089  
acccagcctt caccagccct gtgcgggctc tggggcaga ggtggcagga atggtgctgg 1149  
gcactagtgt tccagggcagc cctgggctaa acaaaagctt gaacttgcca cttcagcggg 1209  
gagatgagag gcaggtgcac tcagctgcac tgcccgagac tigtatgctc tigtacatct 1269  
gtttgttagca cacttgagtt tigtatucc attgacatca aatgtgacaa ttttactaaa 1329  
taaagaattt tggagttagt tacccttgaa aaaaaaaaaa aaaaaaa 1375

<210> 28

<211> 224

<212> PRT

<213> Homo sapiens

<400> 28

Met Ala Pro Pro Ala Ala Pro Gly Arg Asp Arg Val Gly Arg Glu Asp  
1 5 10 15  
Glu Asp Gly Trp Glu Thr Arg Gly Asp Arg Lys Ala Arg Lys Pro Leu  
20 25 30  
Val Glu Lys Lys Arg Arg Ala Arg Ile Asn Glu Ser Leu Gln Glu Leu  
35 40 45  
Arg Leu Leu Leu Ala Gly Ala Glu Val Gln Ala Lys Leu Glu Asn Ala  
50 55 60  
Glu Val Leu Glu Leu Thr Val Arg Arg Val Gln Gly Val Leu Arg Gly  
65 70 75 80  
Arg Ala Arg Glu Glu Gln Leu Gln Ala Glu Ala Ser Glu Arg Phe  
85 90 95  
Ala Ala Gly Tyr Ile Gln Cys Met His Glu Val His Thr Phe Val Ser  
100 105 110  
Thr Cys Gln Ala Ile Asp Ala Thr Val Ala Ala Glu Leu Leu Asn His  
115 120 125  
Leu Leu Glu Ser Met Pro Leu Arg Glu Gly Ser Ser Phe Gln Asp Leu  
130 135 140  
Leu Gly Asp Ala Leu Ala Gly Pro Pro Arg Ala Pro Gly Arg Ser Gly  
145 150 155 160  
Trp Pro Ala Gly Gly Ala Pro Gly Ser Pro Ile Pro Ser Pro Pro Gly  
165 170 175  
Pro Gly Asp Asp Leu Cys Ser Asp Leu Glu Glu Ala Pro Glu Ala Glu  
180 185 190  
Leu Ser Gln Ala Pro Ala Glu Gly Pro Asp Leu Val Pro Ala Ala Leu  
195 200 205  
Gly Ser Leu Thr Thr Ala Gln Ile Ala Arg Ser Val Trp Arg Pro Trp  
210 215 220